

# SEQUENCE LISTING

<110> NISHIDA, Yoshihiro  
OKURA, Takanori  
TANIMOTO, Tadao  
KURIMOTO, Masashi

<120> PEPTIDE

<130>

<150> JP 177,580/98

<151> 1998-6-24

<150> JP 289,044/98

<151> 1998-10-12

<150> JP 365,023/98

<151> 1998-12-22

<160> 33

<210> 1

<211> 108

<212> PRT

<213> Mus musculus

<400> 1

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly  
1 5 10 15

Glu Arg Val Ser Leu Thr Cys (Arg Ala Ser Gln Asp Ile Gly Ser Lys  
20 25 30

Leu Tyr] Trp Leu Gln Gln Glu Pro Asp Gly Thr Phe Lys Arg Leu Ile  
35 40 45

Tyr [Ala Thr Ser Ser Leu Asp Ser] Gly Val Pro Lys Arg Phe Ser Gly  
50 55 60

Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser  
65 70 75 80

Glu Asp Phe Val Asp Tyr Tyr Cys (Leu Gln Tyr Ala Ser Ser Pro Tyr  
85 90 95

Thr] Phe Gly Gly Gly Thr Lys Leu Ala Ile Lys Arg  
100 105

<210> 2

<211> 113

<212> PRT

<213> Mus musculus

<400> 2

Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala  
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr  
20 25 30

Phe Ile Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile  
35 40 45

Gly Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
50 55 60

Arg Asp Lys Ala Thr Leu Thr Val Asp Gln Ser Ser Thr Thr Ala Phe  
65 70 75 80

Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
85 90 95

Ala Arg Gly Leu Arg Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
100 105 110

Ala

<210> 3

<211> 11

<212> PRT

<213> Mus musculus

<400> 3

Arg Ala Ser Gln Asp Ile Gly Ser Lys Leu Tyr  
1 5 10

<210> 4

<211> 7

<212> PRT

<213> Mus musculus

<400> 4

Ala Thr Ser Ser Leu Asp Ser  
1 5

<210> 5

<211> 9

<212> PRT

<213> Mus musculus

<400> 5

Leu Gln Tyr Ala Ser Ser Pro Tyr Thr  
1 5

<210> 6

<211> 10

<212> PRT

<213> Mus musculus

<400> 6

Gly Tyr Ser Phe Thr Asp Tyr Phe Ile Tyr  
1 5 10

<210> 7

<211> 17

<212> PRT

<213> Mus musculus

<400> 7

Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Arg  
1 5 10 15

Asp

<210> 8

<211> 4

<212> PRT

<213> Mus musculus

<400> 8

Gly Leu Arg Phe  
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<210> 9

<211> 237

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificially produced peptide in the form of a single chain  
variable region fragment (scFv) which neutralizes IL-18

<400> 9

Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala  
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr  
20 25 30

Phe Ile Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile  
35 40 45

Gly Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
50 55 60

Arg Asp Lys Ala Thr Leu Thr Val Asp Gln Ser Ser Thr Thr Ala Phe  
65 70 75 80

Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
85 90 95

Ala Arg Gly Leu Arg Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
100 105 110

Ala Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly  
115 120 125

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser  
130 135 140

Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly  
145 150 155 160

Ser Lys Leu Tyr Trp Leu Gln Gln Glu Pro Asp Gly Thr Phe Lys Arg  
165 170 175

Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe  
180 185 190

Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu  
195 200 205

Glu Ser Glu Asp Phe Val Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser  
210 215 220

Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Ala Ile Lys  
225 230 235

<210> 10  
<211> 243  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Artificially produced peptide in the form of a single chain  
variable region fragment (scFv) which neutralizes IL-18

<400> 10  
Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala  
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr  
20 25 30

Phe Ile Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile  
35 40 45

Gly Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
50 55 60

Arg Asp Lys Ala Thr Leu Thr Val Asp Gln Ser Ser Thr Thr Ala Phe  
65 70 75 80

Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
85 90 95

Ala Arg Gly Leu Arg Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
100 105 110

Ala Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly  
115 120 125

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser  
130 135 140

Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly  
145 150 155 160

Ser Lys Leu Tyr Trp Leu Gln Gln Glu Pro Asp Gly Thr Phe Lys Arg  
165 170 175

Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe  
180 185 190

Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu  
195 200 205

Glu Ser Glu Asp Phe Val Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser  
210 215 220

Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Ala Ile Lys His His His  
225 230 235 240

His His His

<210> 11

<211> 324

<212> DNA

<213> Mus musculus

<400> 11

gac atc cag atg acc cag tct cca tcc tcc tta tct gcc tct ctg gga 48  
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly  
1 5 10 15

gaa aga gtc agt ctc act tgt cgg gca agt cag gac att ggt agt aaa 96  
Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly Ser Lys  
20 25 30

tta tac tgg ctt caa cag gaa cca gat gga act ttt aaa cgc ctg atc 144  
Leu Tyr Trp Leu Gln Gln Glu Pro Asp Gly Thr Phe Lys Arg Leu Ile  
35 40 45

tac gcc aca tcc agt tta gat tct ggt gtc ccc aag agg ttc agt ggc 192  
Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly  
50 55 60

agt agg tct ggg tca gat tat tct ctc acc atc agc agc ctt gag tct 240  
Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser  
65 70 75 80

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gaa | gat | ttt | gta | gac | tat | tac | tgt | cta | caa | tat | gct | agt | tct | cgg | tac | 288 |
| Glu | Asp | Phe | Val | Asp | Tyr | Tyr | Cys | Leu | Gln | Tyr | Ala | Ser | Ser | Pro | Tyr |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|-----|
| acg | ttc | gga | ggg | ggg | acc | aag | ctg | gca | ata | aaa | cgg |  |  |  |  | 324 |
| Thr | Phe | Gly | Gly | Gly | Thr | Lys | Leu | Ala | Ile | Lys | Arg |  |  |  |  |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |  |  |  |  |     |

<210> 12  
 <211> 339  
 <212> DNA  
 <213> Mus musculus

|          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| <400> 12 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| gag      | atc | cag | ctg | cag | cag | tct | gga | cct | gag | ctg | gtg | aag | cct | ggg | gct | 48 |
| Glu      | Ile | Gln | Leu | Gln | Gln | Ser | Gly | Pro | Glu | Leu | Val | Lys | Pro | Gly | Ala |    |
| 1        |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| tca | gtg | aag | gtc | tcc | tgt | aag | gct | tct | ggg | tac | tca | ttc | act | gac | tac | 96 |
| Ser | Val | Lys | Val | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Ser | Phe | Thr | Asp | Tyr |    |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ttc | att | tac | tgg | gtg | aag | cag | agc | cat | gga | aag | agc | ctt | gag | tgg | att | 144 |
| Phe | Ile | Tyr | Trp | Val | Lys | Gln | Ser | His | Gly | Lys | Ser | Leu | Glu | Trp | Ile |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gga | gat | att | gat | cct | tat | aat | ggg | gat | act | agt | tac | aac | cag | aag | ttc | 192 |
| Gly | Asp | Ile | Asp | Pro | Tyr | Asn | Gly | Asp | Thr | Ser | Tyr | Asn | Gln | Lys | Phe |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| agg | gac | aag | gcc | aca | ttg | act | ggt | gac | cag | tcc | tcc | acc | aca | gcc | ttc | 240 |
| Arg | Asp | Lys | Ala | Thr | Leu | Thr | Val | Asp | Gln | Ser | Ser | Thr | Thr | Ala | Phe |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| atg | cat | ctc | aac | agc | ctg | aca | tct | gag | gac | tct | gca | gtc | tat | ttc | tgt | 288 |
| Met | His | Leu | Asn | Ser | Leu | Thr | Ser | Glu | Asp | Ser | Ala | Val | Tyr | Phe | Cys |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gca | aga | ggc | cta | cgg | ttc | tgg | ggc | caa | ggg | act | ctg | gtc | act | gtc | tct | 336 |
| Ala | Arg | Gly | Leu | Arg | Phe | Trp | Gly | Gln | Gly | Thr | Leu | Val | Thr | Val | Ser |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |

|     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |
|-----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|-----|
| gca |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 339 |
| Ala |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |

<210> 13  
 <211> 33  
 <212> DNA  
 <213> Mus musculus

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|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|----|
| <400> 13 |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |    |
| cgg      | gca | agt | cag | gac | att | ggg | agt | aaa | tta | tac |  |  |  |  |  | 33 |
| Arg      | Ala | Ser | Gln | Asp | Ile | Gly | Ser | Lys | Leu | Tyr |  |  |  |  |  |    |
| 1        |     |     |     | 5   |     |     |     |     | 10  |     |  |  |  |  |  |    |

<210> 14  
<211> 21  
<212> DNA  
<213> Mus musculus

<400> 14  
gcc aca tcc agt tta gat tct  
Ala Thr Ser Ser Leu Asp Ser  
1 5

21

<210> 15  
<211> 27  
<212> DNA  
<213> Mus musculus

<400> 15  
cta caa tat gct agt tct ccg tac acg  
Leu Gln Tyr Ala Ser Ser Pro Tyr Thr  
1 5

27

<210> 16  
<211> 30  
<212> DNA  
<213> Mus musculus

<400> 16  
ggt tac tca ttc act gac tac ttc att tac  
Gly Tyr Ser Phe Thr Asp Tyr Phe Ile Tyr  
1 5 10

30

<210> 17  
<211> 51  
<212> DNA  
<213> Mus musculus

<400> 17  
gat att gat cct tat aat ggt gat act agt tac aac cag aag ttc agg  
Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Arg  
1 5 10 15

48

gac  
Asp

51

<210> 18  
<211> 12  
<212> DNA  
<213> Mus musculus

<400> 18  
ggc cta cgg ttc  
Gly Leu Arg Phe  
1

12

<210> 19  
<211> 711

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial DNA to code for the amino acid sequence of SEQ  
ID NO:9

<400> 19

|   |     |
|---|-----|
| gag atc cag ctg cag cag tct gga cct gag ctg gtg aag cct ggg gct | 48  |
| Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala |     |
| 1 5 10 15   |     |
| tca gtg aag gtc tcc tgt aag gct tct ggt tac tca ttc act gac tac | 96  |
| Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr |     |
| 20 25 30  |     |
| ttc att tac tgg gtg aag cag agc cat gga aag agc ctt gag tgg att | 144 |
| Phe Ile Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile |     |
| 35 40 45  |     |
| gga gat att gat cct tat aat ggt gat act agt tac aac cag aag ttc | 192 |
| Gly Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe |     |
| 50 55 60  |     |
| agg gac aag gcc aca ttg act gtt gac cag tcc tcc acc aca gcc ttc | 240 |
| Arg Asp Lys Ala Thr Leu Thr Val Asp Gln Ser Ser Thr Thr Ala Phe |     |
| 65 70 75 80   |     |
| atg cat ctc aac agc ctg aca tct gag gac tct gca gtc tat ttc tgt | 288 |
| Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys |     |
| 85 90 95  |     |
| gca aga ggc cta cgg ttc tgg ggc caa ggg act ctg gtc act gtc tct | 336 |
| Ala Arg Gly Leu Arg Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser |     |
| 100 105 110   |     |
| gca ggt gga ggt gga ggc gga tcc ggc gga ggt ggc tct ggc ggt ggc | 384 |
| Ala Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly |     |
| 115 120 125   |     |
| gga tcg gac atc cag atg acc cag tct cca tcc tcc tta tct gcc tct | 432 |
| Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser |     |
| 130 135 140   |     |
| ctg gga gaa aga gtc agt ctc act tgt cgg gca agt cag gac att ggt | 480 |
| Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly |     |
| 145 150 155 160   |     |
| agt aaa tta tac tgg ctt caa cag gaa cca gat gga act ttt aaa cgc | 528 |
| Ser Lys Leu Tyr Trp Leu Gln Gln Glu Pro Asp Gly Thr Phe Lys Arg |     |
| 165 170 175   |     |
| ctg atc tac gcc aca tcc agt tta gat tct ggt gtc ccc aag agg ttc | 576 |
| Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe |     |
| 180 185 190   |     |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| agt | ggc | agt | agg | tct | ggg | tca | gat | tat | tct | ctc | acc | atc | agc | agc | ctt | 624 |
| Ser | Gly | Ser | Arg | Ser | Gly | Ser | Asp | Tyr | Ser | Leu | Thr | Ile | Ser | Ser | Leu |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gag | tct | gaa | gat | ttt | gta | gac | tat | tac | tgt | cta | caa | tat | gct | agt | tct | 672 |
| Glu | Ser | Glu | Asp | Phe | Val | Asp | Tyr | Tyr | Cys | Leu | Gln | Tyr | Ala | Ser | Ser |     |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|-----|
| ccg | tac | acg | ttc | gga | ggg | ggg | acc | aag | ctg | gca | ata | aaa |  |  |  | 711 |
| Pro | Tyr | Thr | Phe | Gly | Gly | Gly | Thr | Lys | Leu | Ala | Ile | Lys |  |  |  |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |  |  |  |     |

<210> 20

<211> 729

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial DNA to code for the amino acid sequence of SEQ  
ID NO:10

<400> 20

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| gag | atc | cag | ctg | cag | cag | tct | gga | cct | gag | ctg | gtg | aag | cct | ggg | gct | 48 |
| Glu | Ile | Gln | Leu | Gln | Gln | Ser | Gly | Pro | Glu | Leu | Val | Lys | Pro | Gly | Ala |    |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| tca | gtg | aag | gtc | tcc | tgt | aag | gct | tct | ggt | tac | tca | ttc | act | gac | tac | 96 |
| Ser | Val | Lys | Val | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Ser | Phe | Thr | Asp | Tyr |    |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ttc | att | tac | tgg | gtg | aag | cag | agc | cat | gga | aag | agc | ctt | gag | tgg | att | 144 |
| Phe | Ile | Tyr | Trp | Val | Lys | Gln | Ser | His | Gly | Lys | Ser | Leu | Glu | Trp | Ile |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gga | gat | att | gat | cct | tat | aat | ggt | gat | act | agt | tac | aac | cag | aag | ttc | 192 |
| Gly | Asp | Ile | Asp | Pro | Tyr | Asn | Gly | Asp | Thr | Ser | Tyr | Asn | Gln | Lys | Phe |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| agg | gac | aag | gcc | aca | ttg | act | gtt | gac | cag | tcc | tcc | acc | aca | gcc | ttc | 240 |
| Arg | Asp | Lys | Ala | Thr | Leu | Thr | Val | Asp | Gln | Ser | Ser | Thr | Thr | Ala | Phe |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| atg | cat | ctc | aac | agc | ctg | aca | tct | gag | gac | tct | gca | gtc | tat | ttc | tgt | 288 |
| Met | His | Leu | Asn | Ser | Leu | Thr | Ser | Glu | Asp | Ser | Ala | Val | Tyr | Phe | Cys |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gca | aga | ggc | cta | cgg | ttc | tgg | ggc | caa | ggg | act | ctg | gtc | act | gtc | tct | 336 |
| Ala | Arg | Gly | Leu | Arg | Phe | Trp | Gly | Gln | Gly | Thr | Leu | Val | Thr | Val | Ser |     |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gca | ggt | gga | ggt | gga | ggc | gga | tcc | ggc | gga | ggt | ggc | tct | ggc | ggt | ggc | 384 |
| Ala | Gly | Gly | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly |     |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gga | tcg | gac | atc | cag | atg | acc | cag | tct | cca | tcc | tcc | tta | tct | gcc | tct | 432 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser  
 130 135 140

ctg gga gaa aga gtc agt ctc act tgt cgg gca agt cag gac att ggt 480  
 Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly  
 145 150 155 160

agt aaa tta tac tgg ctt caa cag gaa cca gat gga act ttt aaa cgc 528  
 Ser Lys Leu Tyr Trp Leu Gln Gln Glu Pro Asp Gly Thr Phe Lys Arg  
 165 170 175

ctg atc tac gcc aca tcc agt tta gat tct ggt gtc ccc aag agg ttc 576  
 Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe  
 180 185 190

agt ggc agt agg tct ggg tca gat tat tct ctc acc atc agc agc ctt 624  
 Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu  
 195 200 205

gag tct gaa gat ttt gta gac tat tac tgt cta caa tat gct agt tct 672  
 Glu Ser Glu Asp Phe Val Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser  
 210 215 220

ccg tac acg ttc gga ggg ggg acc aag ctg gca ata aaa cat cac cat 720  
 Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Ala Ile Lys His His His  
 225 230 235 245

cac cat cac 729  
 His His His

<210> 21  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (73)  
 <223> "Xaa" means an amino acid of isoleucine or threonine.

<400> 21  
 Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn  
 1 5 10 15

Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp  
 20 25 30

Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile  
 35 40 45

Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile  
 50 55 60

Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys Glu Asn Lys Ile

|   |     |     |       |
|---|-----|-----|-------|
| 65  | 70  | 75  | 80    |
| Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys | 85  | 90  | 95    |
| Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys | 100 | 105 | 110   |
| Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu | 115 | 120 | 125   |
| Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu | 130 | 135 | 140   |
| Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp             | 145 | 150 | 155   |
| <210> 22  |     |     |       |
| <211> 157   |     |     |       |
| <212> PRT   |     |     |       |
| <213> Mus Musculus  |     |     |       |
| <220>   |     |     |       |
| <221> UNSURE  |     |     |       |
| <222> (70)  |     |     |       |
| <223> "Xaa" means an amino acid of methionine or threonine.     |     |     |       |
| <400> 22  |     |     |       |
| Asn Phe Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg Asn Ile Asn | 1   | 5   | 10 15 |
| Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe Glu Asp Met | 20  | 25  | 30    |
| Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg Leu Ile Ile | 35  | 40  | 45    |
| Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val Thr Leu Ser | 50  | 55  | 60    |
| Val Lys Asp Ser Lys Xaa Ser Thr Leu Ser Cys Lys Asn Lys Ile Ile | 65  | 70  | 75 80 |
| Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp Ile Gln Ser | 85  | 90  | 95    |
| Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn Lys Met Glu | 100 | 105 | 110   |
| Phe Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys Gln Lys Glu | 115 | 120 | 125   |
| Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp | 130 | 135 | 140   |

Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser  
 145 150 155

<210> 23  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Designed oligonucleotide as sense primer to amplify a cDNA  
 fragment coding for an antibody light chain variable region

<400> 23  
 actagtcgac atgaggrccc ctgctcagwt tyttggmwtc ttg 43

<210> 24  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Designed oligonucleotide as antisense primer to amplify a cDNA  
 fragment coding for an antibody light chain variable region

<400> 24  
 ggatcccggg tggatggtgg gaagatg 27

<210> 25  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Designed oligonucleotide as sense primer to amplify a cDNA  
 fragment coding for an antibody heavy chain variable region

<400> 25  
 actagtcgac atggratgga gckggrtctt tmtctt 36

<210> 26  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Designed oligonucleotide as antisense primer to amplify a cDNA  
 fragment coding for an antibody heavy chain variable region

<400> 26  
 ggatcccggg ccagtggata gacagatg 28

<210> 27  
 <211> 407  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (1)...(407)

<220>  
 <221> sig peptide  
 <222> (1)...(60)

<400> 27

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| atg | agg | gcc | cct | gct | cag | att | ttt | ggc | ttc | ttg | ttg | ctc | ttg | ttt | cca | 48 |
| Met | Arg | Ala | Pro | Ala | Gln | Ile | Phe | Gly | Phe | Leu | Leu | Leu | Leu | Phe | Pro |    |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| ggc | acc | aga | tgt | gac | atc | cag | atg | acc | cag | tct | cca | tcc | tcc | tta | tct | 96 |
| Gly | Thr | Arg | Cys | Asp | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Ser | Leu | Ser |    |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gcc | tct | ctg | gga | gaa | aga | gtc | agt | ctc | act | tgt | cgg | gca | agt | cag | gac | 144 |
| Ala | Ser | Leu | Gly | Glu | Arg | Val | Ser | Leu | Thr | Cys | Arg | Ala | Ser | Gln | Asp |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| att | ggc | agt | aaa | tta | tac | tgg | ctt | caa | cag | gaa | cca | gat | gga | act | ttt | 192 |
| Ile | Gly | Ser | Lys | Leu | Tyr | Trp | Leu | Gln | Gln | Glu | Pro | Asp | Gly | Thr | Phe |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aaa | cgc | ctg | atc | tac | gcc | aca | tcc | agt | tta | gat | tct | ggc | gtc | ccc | aag | 240 |
| Lys | Arg | Leu | Ile | Tyr | Ala | Thr | Ser | Ser | Leu | Asp | Ser | Gly | Val | Pro | Lys |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| agg | ttc | agt | ggc | agt | agg | tct | ggg | tca | gat | tat | tct | ctc | acc | atc | agc | 288 |
| Arg | Phe | Ser | Gly | Ser | Arg | Ser | Gly | Ser | Asp | Tyr | Ser | Leu | Thr | Ile | Ser |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| agc | ctt | gag | tct | gaa | gat | ttt | gta | gac | tat | tac | tgt | cta | caa | tat | gct | 336 |
| Ser | Leu | Glu | Ser | Glu | Asp | Phe | Val | Asp | Tyr | Tyr | Cys | Leu | Gln | Tyr | Ala |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| agt | tct | ccg | tac | acg | ttc | gga | ggg | ggg | acc | aag | ctg | gca | ata | aaa | cgg | 384 |
| Ser | Ser | Pro | Tyr | Thr | Phe | Gly | Gly | Gly | Thr | Lys | Leu | Ala | Ile | Lys | Arg |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |

|     |     |     |     |     |     |     |    |  |  |  |  |  |  |  |  |     |
|-----|-----|-----|-----|-----|-----|-----|----|--|--|--|--|--|--|--|--|-----|
| gct | gat | gct | gca | cca | act | gta | tc |  |  |  |  |  |  |  |  | 407 |
| Ala | Asp | Ala | Ala | Pro | Thr | Val |    |  |  |  |  |  |  |  |  |     |
|     |     | 130 |     |     |     | 135 |    |  |  |  |  |  |  |  |  |     |

<210> 28  
 <211> 412  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (1)...(412)

<220>

<221> sig peptide

<222> (1)...(60)

<400> 28

|   |    |
|---|----|
| atg gga tgg agc ggg atc ttt ctc ttc ctc ctg tca gga cct aca ggt | 48 |
| Met Gly Trp Ser Gly Ile Phe Leu Phe Leu Leu Ser Gly Pro Thr Gly |    |
| 1 5 10 15   |    |

|   |    |
|---|----|
| gtc cac tct gag atc cag ctg cag cag tct gga cct gag ctg gtg aag | 96 |
| Val His Ser Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys |    |
| 20 25 30  |    |

|   |     |
|---|-----|
| cct ggg gct tca gtg aag gtc tcc tgt aag gct tct ggt tac tca ttc | 144 |
| Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe |     |
| 35 40 45  |     |

|   |     |
|---|-----|
| act gac tac ttc att tac tgg gtg aag cag agc cat gga aag agc ctt | 192 |
| Thr Asp Tyr Phe Ile Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu |     |
| 50 55 60  |     |

|   |     |
|---|-----|
| gag tgg att gga gat att gat cct tat aat ggt gat act agt tac aac | 240 |
| Glu Trp Ile Gly Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn |     |
| 65 70 75 80   |     |

|   |     |
|---|-----|
| cag aag ttc agg gac aag gcc aca ttg act gtt gac cag tcc tcc acc | 288 |
| Gln Lys Phe Arg Asp Lys Ala Thr Leu Thr Val Asp Gln Ser Ser Thr |     |
| 85 90 95  |     |

|   |     |
|---|-----|
| aca gcc ttc atg cat ctc aac agc ctg aca tct gag gac tct gca gtc | 336 |
| Thr Ala Phe Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val |     |
| 100 105 110   |     |

|   |     |
|---|-----|
| tat ttc tgt gca aga ggc cta cgg ttc tgg ggc caa ggg act ctg gtc | 384 |
| Tyr Phe Cys Ala Arg Gly Leu Arg Phe Trp Gly Gln Gly Thr Leu Val |     |
| 115 120 125   |     |

|                                       |     |
|---------------------------------------|-----|
| act gtc tct gca gcc aaa acg aca ccc c | 412 |
| Thr Val Ser Ala Ala Lys Thr Thr Pro   |     |
| 130 135                               |     |

<210> 29

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide as sense primer to amplify a DNA fragment containing the nucleotide sequence of SEQ ID NO:12

<400> 29

|                               |    |
|-------------------------------|----|
| gtcatatgga gatccagctg cagcagt | 27 |
|-------------------------------|----|

<210> 30

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide as antisense primer to amplify a DNA fragment containing the nucleotide sequence of SEQ ID NO:12

<400> 30

gaggatccgc ctccacctcc acctgcagag acagtgacca gag

43

<210> 31

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide as sense primer to amplify a DNA fragment containing a part of the nucleotide sequence of SEQ ID NO:11

<400> 31

tggatccggc ggaggtggct ctggcgggtgg cggatcggac atccagatga

50

<210> 32

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide as antisense primer to amplify a DNA fragment containing a part of the nucleotide sequence of SEQ ID NO:11

<400> 32

ccggatcctt attttattgc cagcttggtc c

31

<210> 33

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide as antisense primer to amplify a DNA fragment containing a part of the nucleotide sequence of SEQ ID NO:11

<400> 33

tggatcctta gtgatgggtga tggatgatgtt ttattgccag cttgg

45